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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/052,798

DATE: 02/06/2002
 TIME: 15:49:38

Input Set : N:\Crf3\RULE60\10052798.raw
 Output Set: N:\CRF3\02062002\J052798.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.
 6 Ashkenazi, Avi J.
 7 Chuntharapai, Anan
 8 Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

12 (iii) NUMBER OF SEQUENCES: 14

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
 16 (B) STREET: 1 DNA Way
 17 (C) CITY: South San Francisco
 18 (D) STATE: California
 19 (E) COUNTRY: USA
 20 (F) ZIP: 94080

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: WinPatIn (Genentech)

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/052,798
 C--> 30 (B) FILING DATE: 02-Nov-2001
 31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/09/079,029
 35 (B) FILING DATE:

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Marschang, Diane L.
 40 (B) REGISTRATION NUMBER: 35,600
 41 (C) REFERENCE/DOCKET NUMBER: P1101R2

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 650/225-5416
 45 (B) TELEFAX: 650/952-9881

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 411 amino acids
 50 (B) TYPE: Amino Acid
 51 (D) TOPOLOGY: Linear

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 56 1 5 10 15
 58 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro

ENTERED

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59		20		25		30
61	Gly Leu Arg Val	Pro Lys Thr Leu Val	Leu Val Val Ala Ala Val			
62		35		40		45
64	Leu Leu Leu Val	Ser Ala Glu Ser Ala	Leu Ile Thr Gln Gln Asp			
65		50		55		60
67	Leu Ala Pro Gln	Gln Arg Ala Ala Pro	Gln Gln Lys Arg Ser Ser			
68		65		70		75
70	Pro Ser Glu Gly	Leu Cys Pro Pro Gly	His His Ile Ser Glu Asp			
71		80		85		90
73	Gly Arg Asp Cys	Ile Ser Cys Lys Tyr	Gly Gln Asp Tyr Ser Thr			
74		95		100		105
76	His Trp Asn Asp	Leu Leu Phe Cys Leu	Arg Cys Thr Arg Cys Asp			
77		110		115		120
79	Ser Gly Glu Val	Glu Leu Ser Pro Cys	Thr Thr Thr Arg Asn Thr			
80		125		130		135
82	Val Cys Gln Cys	Glu Glu Gly Thr Phe	Arg Glu Glu Asp Ser Pro			
83		140		145		150
85	Glu Met Cys Arg	Lys Cys Arg Thr Gly	Cys Pro Arg Gly Met Val			
86		155		160		165
88	Lys Val Gly Asp	Cys Thr Pro Trp Ser	Asp Ile Glu Cys Val His			
89		170		175		180
91	Lys Glu Ser Gly	Ile Ile Ile Gly Val	Thr Val Ala Ala Val Val			
92		185		190		195
94	Leu Ile Val Ala	Val Phe Val Cys Lys	Ser Leu Leu Trp Lys Lys			
95		200		205		210
97	Val Leu Pro Tyr	Leu Lys Gly Ile Cys	Ser Gly Gly Gly Gly Asp			
98		215		220		225
100	Pro Glu Arg Val	Asp Arg Ser Ser Gln	Arg Pro Gly Ala Glu Asp			
101		230		235		240
103	Asn Val Leu Asn	Glu Ile Val Ser Ile	Leu Gln Pro Thr Gln Val			
104		245		250		255
106	Pro Glu Gln Glu	Met Glu Val Gln Glu	Pro Ala Glu Pro Thr Gly			
107		260		265		270
109	Val Asn Met Leu	Ser Pro Gly Glu Ser	Glu His Leu Leu Glu Pro			
110		275		280		285
112	Ala Glu Ala Glu	Arg Ser Gln Arg Arg	Arg Leu Leu Val Pro Ala			
113		290		295		300
115	Asn Glu Gly Asp	Pro Thr Glu Thr Leu	Arg Gln Cys Phe Asp Asp			
116		305		310		315
118	Phe Ala Asp Leu	Val Pro Phe Asp Ser	Trp Glu Pro Leu Met Arg			
119		320		325		330
121	Lys Leu Gly Leu	Met Asp Asn Glu Ile	Lys Val Ala Lys Ala Glu			
122		335		340		345
124	Ala Ala Gly His	Arg Asp Thr Leu Tyr	Thr Met Leu Ile Lys Trp			
125		350		355		360
127	Val Asn Lys Thr	Gly Arg Asp Ala Ser	Val His Thr Leu Leu Asp			
128		365		370		375
130	Ala Leu Glu Thr	Leu Gly Glu Arg Leu	Ala Lys Gln Lys Ile Glu			
131		380		385		390

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133  Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
134                                395                        400      405
W--> 136  Ala Asp Ser Ala Xaa Ser
137                                410 411
139 (2) INFORMATION FOR SEQ ID NO: 2:
141   (i) SEQUENCE CHARACTERISTICS:
142       (A) LENGTH: 1799 base pairs
143       (B) TYPE: Nucleic Acid
144       (C) STRANDEDNESS: Single
145       (D) TOPOLOGY: Linear
147   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
150  CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50
152  GCGCCCACAA AATACACCGA CGATGCCCCG TCTACTTTAA GGGCTGAAAC 100
154  CCACGGGCTT GAGAGACTAT AAGAGCGTTC CCTACCGCC  ATG GAA 145
155                                     Met Glu
156                                     1
158  CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
159  Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
160          5                      10                      15
162  AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
163  Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
164          20                      25
166  AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
167  Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
168          30                      35                      40
170  GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
171  Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
172          45                      50
174  CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
175  Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
176  55                      60                      65
178  GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
179  Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
180          70                      75                      80
182  TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
183  Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
184          85                      90
186  TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
187  Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
188          95                      100                      105
190  TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
191  Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
192          110                      115
194  GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
195  Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
196  120                      125                      130
198  AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
199  Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
200          135                      140                      145

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202  GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
203  Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
204          150                      155
206  GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
207  Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
208          160                      165                      170
210  CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
211  Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
212          175                      180
214  ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
215  Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
216  185                      190                      195
218  GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
219  Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
220          200                      205                      210
222  GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
223  Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
224          215                      220
226  GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
227  Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
228          225                      230                      235
230  GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
231  Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
232          240                      245
234  TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
235  Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
236  250                      255                      260
238  CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
239  Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
240          265                      270                      275
242  CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
243  Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
244          280                      285
246  GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
247  Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
248          290                      295                      300
250  GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
251  Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
252          305                      310
254  GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
255  Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
256  315                      320                      325
258  CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
259  Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
260          330                      335                      340
262  GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
263  Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
264          345                      350
266  TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237

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267 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
268      355                      360                      365
270 GAT GCC TCT GTC CAC ACC CTG GAT GCC TTG GAG ACG 1276
271 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
272      370                      375
274 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
275 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
276      380                      385                      390
278 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
279 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
280      395                      400                      405
282 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
W--> 283 Ala Asp Ser Ala Xaa Ser
W--> 284      410 411
286 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
288 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
290 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTTACTGCAC 1550
292 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600
294 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTGTT TGGGATGTCA 1650
296 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700
298 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAAG 1750
300 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799
302 (2) INFORMATION FOR SEQ ID NO: 3:
304     (i) SEQUENCE CHARACTERISTICS:
305         (A) LENGTH: 70 base pairs
306         (B) TYPE: Nucleic Acid
307         (C) STRANDEDNESS: Single
308         (D) TOPOLOGY: Linear
310     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
313 GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
315 GCTAAAGCTG AGGCAGCGGG 70
317 (2) INFORMATION FOR SEQ ID NO: 4:
319     (i) SEQUENCE CHARACTERISTICS:
320         (A) LENGTH: 29 base pairs
321         (B) TYPE: Nucleic Acid
322         (C) STRANDEDNESS: Single
323         (D) TOPOLOGY: Linear
325     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
328 ATCAGGGACT TTCCGCTGGG GACTTTCCG 29
330 (2) INFORMATION FOR SEQ ID NO: 5:
332     (i) SEQUENCE CHARACTERISTICS:
333         (A) LENGTH: 30 base pairs
334         (B) TYPE: Nucleic Acid
335         (C) STRANDEDNESS: Single
336         (D) TOPOLOGY: Linear
338     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
341 AGGATGGGAA GTGTGTGATA TATCCTTGAT 30
343 (2) INFORMATION FOR SEQ ID NO: 6:
345     (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\02062002\J052798..raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2